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Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365

Trp Ser Asp Arg Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400

Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415

Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe

Sub
DI
at
cont

465 470 475 480
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
 485 490 495
 Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
 500 505 510
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
 515 520 525
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
 530 535 540
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
 545 550 555 560
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
 565 570 575
 Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
 580 585 590
 Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
 595 600 605
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
 610 615 620
 Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln
 625 630 635 640
 Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
 660 665 670
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
 675 680 685
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
 690 695 700
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
 705 710 715 720
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr

Sub
 D1
 cont

725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
 785 790 795 800
 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
 805 810 815
 Leu Thr Met Tyr Ala
 820

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1 5 10 15
Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Gly Lys Thr Thr
20 25 30
Glu Ala Gly Gly Gly His Pro Gly Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45
Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60
His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Leu Asp Pro Glu Phe
65 70 75 80
Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95
Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110
Ile Gly Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Asp Leu Gly Asp
115 120 125
Cys Trp Leu Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Glu Arg Leu
130 135 140
Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Thr Glu Asn Tyr Ala
145 150 155 160
Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Asp Trp Val Asp Val
165 170 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
 180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
 195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
 210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Thr Glu Phe Phe Glu
 225 230 235 240

Ile Lys Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Arg Lys Ala Ile
 245 250 255

AI cont Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
 260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
 275 280 285

Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Arg Asp Ser Asp Leu
 290 295 300

Asp Pro Arg Ala Ser Asp Asp Arg Pro Ser Arg Thr Ile Val Pro Val
 305 310 315 320

Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
 340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365

Trp Ser Asp Gly Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400

Tyr Asp Asp Phe Val Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415

Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
 435 440 445
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
 450 455 460
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
 465 470 475 480
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
 485 490 495
 Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
 500 505 510
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
 515 520 525
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
 530 535 540
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
 545 550 555 560
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
 565 570 575
 Lys Arg Asn Leu Ser Glu Glu Ala Glu Asn Thr Ile Ser Val Asp Arg
 580 585 590
 Pro Val Lys Lys Lys Lys Asn Lys Pro Ile Ile Phe Val Ser Asp Arg
 595 600 605
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ala Glu Glu Gly
 610 615 620
 Lys Asp Lys Thr Gly Pro Asp Lys Gln Gly Glu Ser Pro Gln Pro Arg
 625 630 635 640
 Pro Gly His Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Arg Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
 660 665 670
 Leu Lys Asn Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
 675 680 685

Side
 DI
 Cal
 cont

Thr Gln Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
 690 695 700
 Asp Thr Asp Gly Ser Gly Arg Leu Asn Leu Gln Glu Phe His His Leu
 705 710 715 720
 Trp Lys Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
 725 730 735
 Asp His Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Ser Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
 785 790 795 800
 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
 805 810 815
 Leu Thr Met Tyr Ala
 820

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/note= "FIGURE 3 -PIG"

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Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
1 5 10 15

Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
20 25 30

Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
35 40 45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
50 55 60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65 70 75 80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110

Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
115 120 125

Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
130 135 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145 150 155 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
165 170 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
245 250 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Asp Leu Ile Ala
275 280 285

Arg Met Val Arg Asn Met Glu Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Thr Ile Val Pro Val
305 310 315 320

Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365

Sub
D1
cont

Trp Ser Asp Ser Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Asp Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415
 Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Thr Gly Arg
 435 440 445
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
 450 455 460
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
 465 470 475 480
 Leu Val Ala Leu Met Gln Arg Asn Arg Arg Lys Asp Arg Lys Leu Gly
 485 490 495
 Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
 500 505 510
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
 515 520 525
 Ala Ser Lys Ala Arg Ser Arg Thr Tyr Ile Asn Met Arg Glu Val Ser
 530 535 540
 Glu Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
 545 550 555 560
 Tyr Glu Pro His Gln Glu Gly Glu Phe Met Leu Arg Val Phe Ser Glu
 565 570 575
 Lys Arg Lys Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
 580 585 590
 Pro Val Arg Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
 595 600 605
 Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
 610 615 620

Sub
 DI
 CH
 cont

Gln Asp Lys Thr Ser Pro Asp Lys Gln Glu Lys Ser Pro Lys Pro Glu
 625 630 635 640
 Pro Ser Asn Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
 645 650 655
 Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
 660 665 670
 Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
 675 680 685
 Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
 690 695 700
 Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
 705 710 715 720
 Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
 725 730 735
 Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
 740 745 750
 Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
 755 760 765
 Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
 770 775 780
 Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
 785 790 795 800
 Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
 805 810 815
 Leu Thr Met Tyr Ala
 820

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<223> /label= ALU

/note= "FIGURE 3 -COW"

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Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu

1

5

10

15

Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr

20

25

30

Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser

35

40

45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu

50 55 60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65 70 75 80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
85 90 95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
100 105 110

Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
115 120 125

Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
130 135 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145 150 155 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
165 170 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
245 250 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Glu
275 280 285

Arg Met Val Arg Asn Met Asp Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Met Ile Val Pro Val

Sub
DI
cont

305 310 315 320
 Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
 325 330 335
 Ser Val Thr Gly Leu Glu Glu Ala Leu Tyr Lys Gly Glu Lys Val Lys
 340 345 350
 Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
 355 360 365
 Trp Ser Asp Ser Trp Lys Asp Trp Ser Tyr Val Asp Lys Asp Glu Lys
 370 375 380
 Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
 385 390 395 400
 Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
 405 410 415
 Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
 420 425 430
 Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
 435 440 445
 Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
 450 455 460
 Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
 465 470 475 480
 Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
 485 490 495
 Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
 500 505 510
 Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
 515 520 525
 Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
 530 535 540
 Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
 545 550 555 560
 Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu

Sub
 D1
 Cont

565

570

575

Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
580 585 590

Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605

Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
610 615 620

Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln
625 630 635 640

Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
645 650 655

Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
660 665 670

Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
675 680 685

Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
690 695 700

Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
705 710 715 720

Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
725 730 735

Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
740 745 750

Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
755 760 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
770 775 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785 790 795 800

Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
805 810 815

Leu Thr Met Tyr Ala

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 <212> DNA
 <213> Homo sapiens

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21

<210> 12
 <211> 20
 <212> DNA
 <213> Homo sapiens

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<210> 13
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 <212> DNA
 <213> Homo sapiens

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<223> /label= Table 1

<400> 13
ttgctgttcc tcactttcct g

21

<210> 14
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<212> DNA
<213> Homo sapiens

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gtttcatctg ctgcttcggt

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<210> 15
<211> 20
<212> DNA
<213> Homo sapiens

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<223> /label= Table 1

<400> 15
ctgggtcagg catacatggt

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<210> 16
<211> 22
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(22)
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<400> 16
ttcttttatgt ggaccctgag tt

22

<210> 17
<211> 19

<212> DNA
<213> Homo sapiens

<220>
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acgaactgga tggggaact

19

<210> 18
<211> 20
<212> DNA
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<220>
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<222> (1)..(20)
<223> /label= Table 3

<400> 18
ttcagttacct cccgttcacc

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<210> 19
<211> 20
<212> DNA
<213> Homo sapiens

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<222> (1)..(20)
<223> /label= Table 3

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gatgcttgag ccaggaaaac

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<210> 20
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<212> DNA
<213> Homo sapiens

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<222> (1)..(22)
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ctttccttga aggtagctgt at

22

<210> 21

<211> 20

<212> DNA

<213> Homo sapiens

<220>

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<212> DNA

<213> Homo sapiens

<220>

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<223> /label= Table 3

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<210> 23

<211> 20

<212> DNA

<213> Homo sapiens

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<223> /label= Table 3

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<210> 24

<211> 20

<212> DNA

<213> Homo sapiens

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tggaagtagg agagtgggca

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<210> 25
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<212> DNA
<213> Homo sapiens

<220>
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<223> /label= Table 3

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gggtagatgg gtgggaagtt

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<210> 26
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<212> DNA
<213> Homo sapiens

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<223> /label= Table 3

<400> 26
gaggaatgtg gaggaaggac

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<210> 27
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<212> DNA
<213> Homo sapiens

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<400> 27
ttcctgtgag tgaggtctcg

20

<210> 28
<211> 20

<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(20)
<223> /label= Table 3

<400> 28
ggaactctgt gaccccaa

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<210> 29
<211> 20
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(20)
<223> /label= Table 3

<400> 29
tcctcaaaca aaacattcgc

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<210> 30
<211> 20
<212> DNA
<213> Homo sapiens

<220>
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<223> /label= Table 3

<400> 30
gttcctaca ttctccatcg

20

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<211> 21
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (1)..(21)
<223> /label= Table 3

<400> 31

ggtattttcaa cccagaccct t

21

<210> 32

<211> 21

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(21)

<223> /label= Table 3

<400> 32

aatgggttct ctggttactg c

21

<210> 33

<211> 21

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(21)

<223> /label= Table 3

<400> 33

agcacgaaaa gcaaagataa a

21

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